



-1-

SEQUENCE LISTING

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<110> Oko, Richard  
Sutovsky, Peter

<120> PT32 Sperm Protein, Sperm c-Yes, Oocyte Cytoplasmic c-Yes, and Uses  
Thereof

<130> 1669.0050001

<140> US 09/864,291

<141> 2001-05-25

<150> US 60/206,979

<151> 2000-05-25

AI <150> CA 2,307,128

<151> 2000-05-25

<160> 20

<170> PatentIn version 3.1

<210> 1

<211> 5

<212> PRT

<213> mammalian

<400> 1

Pro Pro Pro Gly Tyr  
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<210> 2

<211> 5

<212> PRT

<213> mammalian

<400> 2

Leu Pro Pro Ala Tyr  
1 5

<210> 3

<211> 7

<212> PRT

<213> mammalian

<220>

<221> misc\_feature

<222> (3)..(3)

<223> X may be any amino acid residue

<220>

<221> misc\_feature

<222> (6)..(6)

<223> X may be any amino acid residue

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<211> 1413

<212> DNA

<213> mammalian

<220>

A1

<221> CDS

<222> (36)..(974)

<223>

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1 5	
cac acc gag agc cgt cgt ggg gcc ctc atc ccc tct ggc gaa agt gtc	101
His Thr Glu Ser Arg Arg Gly Ala Leu Ile Pro Ser Gly Glu Ser Val	
10 15 20	
ttg aag cag tgt gag gat gtg gac ctc tgc ttc cta cag aaa cca gtg	149
Leu Lys Gln Cys Glu Asp Val Asp Leu Cys Phe Leu Gln Lys Pro Val	
25 30 35	
gaa tcc tat ctc ttt aat ggc aca aag aaa gga acg ttg ttt ctc act	197
Glu Ser Tyr Leu Phe Asn Gly Thr Lys Lys Gly Thr Leu Phe Leu Thr	
40 45 50	
tca tac cgg gtg gtc ttc gtg act tca cac tta gtc aat gac ccc atg	245
Ser Tyr Arg Val Val Phe Val Thr Ser His Leu Val Asn Asp Pro Met	
55 60 65 70	
ctt tct ttt atg atg ccg ttt ggc ctg atg agt gac tgc acc att gaa	293
Leu Ser Phe Met Met Pro Phe Gly Leu Met Ser Asp Cys Thr Ile Glu	
75 80 85	
caa cca att ttt gcc ccc aac tac att aaa gga acc att cag gca gct	341
Gln Pro Ile Phe Ala Pro Asn Tyr Ile Lys Gly Thr Ile Gln Ala Ala	
90 95 100	
cca ggt ggt ggc tgg gaa gga caa gct gtt ttt aag tta tcc ttc agg	389
Pro Gly Gly Gly Trp Glu Gly Gln Ala Val Phe Lys Leu Ser Phe Arg	
105 110 115	
aaa gga ggt gcc atc gaa ttt gcc caa ctg atg gta aaa gct gcc tct	437
Lys Gly Gly Ala Ile Glu Phe Ala Gln Leu Met Val Lys Ala Ala Ser	
120 125 130	
gct gct gcc aga gga att cca ctt gga agt gta aat tac tgg ttc gac	485
Ala Ala Ala Arg Gly Ile Pro Leu Gly Ser Val Asn Tyr Trp Phe Asp	
135 140 145 150	
act tca gga ctg tac ata att act gtc cca ggg gct gca gtg tgc tcc	533
Thr Ser Gly Leu Tyr Ile Ile Thr Val Pro Gly Ala Ala Val Cys Ser	
155 160 165	
tca cag aca cct tgt cca gca tat cca att gtg atc tat gga ccc cca	581
Ser Gln Thr Pro Cys Pro Ala Tyr Pro Ile Val Ile Tyr Gly Pro Pro	
170 175 180	
cca cca gga tat aca gtc caa cca ggg gaa tat gga act cca cca gaa	629
Pro Pro Gly Tyr Thr Val Gln Pro Gly Glu Tyr Gly Thr Pro Pro Glu	
185 190 195	
gga tat gga gcc caa cca ggg gga tat gga gcc cca cct atg gga tat	677

A1

Gly Tyr Gly Ala Gln Pro Gly Gly Tyr Gly Ala Pro Pro Met Gly Tyr  
 200 205 210

gga gcc ccg cct gtg gga tat gga gtc cca cct ggg gga tat gga gtc 725  
 Gly Ala Pro Pro Val Gly Tyr Gly Val Pro Pro Gly Gly Tyr Gly Val  
 215 220 225 230

cca cct ggg gga tat gga gtc cca cct ggg gga tat gga gcc cca cct 773  
 Pro Pro Gly Gly Tyr Gly Val Pro Pro Gly Tyr Gly Ala Pro Pro  
 235 240 245

ggg gga tat gga gtc cca cct ggg gga tat ggt gcc cca cct ggg gga 821  
 Gly Gly Tyr Gly Val Pro Pro Gly Gly Tyr Gly Ala Pro Pro Gly Gly  
 250 255 260

tat gga gcc cca cct gca gga tat gga gcc cca cca gct gga aat gaa 869  
 Tyr Gly Ala Pro Pro Ala Gly Tyr Gly Ala Pro Pro Ala Gly Asn Glu  
 265 270 275

gcc cta ccc cct gca tat gaa gct cca tct gct gga aat aca gct gcc 917  
 Ala Leu Pro Pro Ala Tyr Glu Ala Pro Ser Ala Gly Asn Thr Ala Ala  
 280 285 290

tct cac aga tct atg aca gct cag cag gag act tct ctt ccc act acc 965  
 Ser His Arg Ser Met Thr Ala Gln Gln Glu Thr Ser Leu Pro Thr Thr  
 295 300 305 310

tca tct tct taggtccatt taccaccttc tcagagttaa accttgaaga 1014  
 Ser Ser Ser

ctcaccaagc aaagggcacc ctaaaactga agtcacagta agaaggaaga cccaggtgcc 1074

cagtggtagg aggtgttcgt gtgcacgcag tggctctgatc ttctccacac acctgtgagg 1134

tctgtgcct caaaacagat gaaggtgaga agacgactcc tgttctcaag gaaggaagat 1194

gcttgaaaac agactgcaag ccaactagag agagagagat gtgaagtggc acataaaaca 1254

gcttggggat ggagactgac tctctttaga aaacaggcct tctccctgcc tctgacctga 1314

gcagaaaaga gaaatcgctg gaaccaaaga gctaggggtca ccctgcttag acgccctcga 1374

ttaaagcctg cttgctgttg cataaaaaaaaa aaaaaaaaaa 1413

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<211> 313

<212> PRT

<213> mammalian

<400> 5

Met Ala Val Asn Gln Ser His Thr Glu Ser Arg Arg Gly Ala Leu Ile  
 1 5 10 15

Pro Ser Gly Glu Ser Val Leu Lys Gln Cys Glu Asp Val Asp Leu Cys  
20 25 30

Phe Leu Gln Lys Pro Val Glu Ser Tyr Leu Phe Asn Gly Thr Lys Lys  
35 40 45

Gly Thr Leu Phe Leu Thr Ser Tyr Arg Val Val Phe Val Thr Ser His  
50 55 60

Leu Val Asn Asp Pro Met Leu Ser Phe Met Met Pro Phe Gly Leu Met  
65 70 75 80

Ser Asp Cys Thr Ile Glu Gln Pro Ile Phe Ala Pro Asn Tyr Ile Lys  
85 90 95

Gly Thr Ile Gln Ala Ala Pro Gly Gly Gly Trp Glu Gly Gln Ala Val  
100 105 110

Phe Lys Leu Ser Phe Arg Lys Gly Gly Ala Ile Glu Phe Ala Gln Leu  
115 120 125

Met Val Lys Ala Ala Ser Ala Ala Ala Arg Gly Ile Pro Leu Gly Ser  
130 135 140

Val Asn Tyr Trp Phe Asp Thr Ser Gly Leu Tyr Ile Ile Thr Val Pro  
145 150 155 160

Gly Ala Ala Val Cys Ser Ser Gln Thr Pro Cys Pro Ala Tyr Pro Ile  
165 170 175

Val Ile Tyr Gly Pro Pro Pro Pro Gly Tyr Thr Val Gln Pro Gly Glu  
180 185 190

Tyr Gly Thr Pro Pro Glu Gly Tyr Gly Ala Gln Pro Gly Gly Tyr Gly  
195 200 205

Ala Pro Pro Met Gly Tyr Gly Ala Pro Pro Val Gly Tyr Gly Val Pro  
210 215 220

Pro Gly Gly Tyr Gly Val Pro Pro Gly Gly Tyr Gly Val Pro Pro Gly  
225 230 235 240

Gly Tyr Gly Ala Pro Pro Gly Gly Tyr Gly Val Pro Pro Gly Gly Tyr  
245 250 255

Gly Ala Pro Pro Gly Gly Tyr Gly Ala Pro Pro Ala Gly Tyr Gly Ala  
260 265 270

A1

Pro Pro Ala Gly Asn Glu Ala Leu Pro Pro Ala Tyr Glu Ala Pro Ser  
275 280 285

Ala Gly Asn Thr Ala Ala Ser His Arg Ser Met Thr Ala Gln Gln Glu  
290 295 300

Thr Ser Leu Pro Thr Thr Ser Ser Ser  
305 310

<210> 6

<211> 24

<212> PRT

<213> mammalian

<400> 6

Thr Ser Tyr Arg Val Val Phe Val Thr Ser His Leu Val Asn Asp Pro  
1 5 10 15

Met Leu Ser Phe Met Met Pro Phe  
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A7  
<210> 7

<211> 16

<212> PRT

<213> mammalian

<400> 7

Asn Glu Ala Leu Pro Pro Ala Tyr Glu Ala Pro Ser Ala Gly Asn Thr  
1 5 10 15

<210> 8

<211> 4

<212> PRT

<213> mammalian

<220>

<221> misc\_feature

<222> (3)..(3)

<223> X may be any amino acid

<400> 8

Pro Pro Xaa Tyr  
1

<210> 9

<211> 239

<212> PRT

<213> Bos sp.

<400> 9

Met Pro Phe Gly Leu Met Ser Asp Cys Thr Ile Glu Gln Pro Ile Phe  
1 5 10 15

Ala Pro Asn Tyr Ile Lys Gly Thr Ile Gln Ala Ala Pro Gly Gly Gly  
20 25 30

Trp Glu Gly Gln Ala Val Phe Lys Leu Ser Phe Arg Lys Gly Gly Ala  
35 40 45

Ile Glu Phe Ala Gln Leu Met Val Lys Ala Ala Ser Ala Ala Ala Arg  
50 55 60

Gly Ile Pro Leu Gly Ser Val Asn Tyr Trp Phe Asp Thr Ser Gly Leu  
65 70 75 80

Tyr Ile Ile Thr Val Pro Gly Ala Ala Val Cys Ser Ser Gln Thr Pro  
85 90 95

Cys Pro Ala Tyr Pro Ile Val Ile Tyr Gly Pro Pro Pro Pro Gly Tyr  
100 105 110

Thr Val Gln Pro Gly Glu Tyr Gly Thr Pro Pro Glu Gly Tyr Gly Ala  
115 120 125

Gln Pro Gly Gly Tyr Gly Ala Pro Pro Met Gly Tyr Gly Ala Pro Pro  
130 135 140

Val Gly Tyr Gly Val Pro Pro Gly Gly Tyr Gly Val Pro Pro Gly Gly  
145 150 155 160

A7

Tyr Gly Val Pro Pro Gly Gly Tyr Gly Ala Pro Pro Gly Gly Tyr Gly  
165 170 175

Val Pro Pro Gly Gly Tyr Gly Ala Pro Pro Gly Gly Tyr Gly Ala Pro  
180 185 190

Pro Ala Gly Tyr Gly Ala Pro Pro Ala Gly Asn Glu Ala Leu Pro Pro  
195 200 205

Ala Tyr Glu Ala Pro Ser Ala Gly Asn Thr Ala Ala Ser His Arg Ser  
210 215 220

Met Thr Ala Gln Gln Glu Thr Ser Leu Pro Thr Thr Ser Ser Ser  
225 230 235

<210> 10

<211> 225

<212> PRT

<213> Homo sapiens

A7  
<400> 10

Met Pro Phe Asp Leu Met Thr Asn Leu Thr Val Glu Gln Pro Val Phe  
1 5 10 15

Ala Ala Asn Phe Ile Lys Gly Thr Ile Gln Ala Ala Pro Tyr Gly Gly  
20 25 30

Trp Glu Gly Gln Ala Thr Phe Lys Leu Val Phe Arg Asn Gly Asp Ala  
35 40 45

Ile Glu Phe Ala Gln Leu Met Val Lys Ala Ala Ser Ala Val Ile Val  
50 55 60

Tyr Gly Ala Pro Pro Ala Gly Tyr Gly Ala Pro Pro Pro Gly Tyr Gly  
65 70 75 80

Ala Pro Pro Ala Gly Tyr Gly Ala Gln Pro Val Gly Asn Glu Gly Pro  
85 90 95

Pro Val Gly Tyr Arg Ala Ser Pro Val Arg Tyr Gly Ala Pro Pro Leu  
100 105 110

Gly Tyr Gly Ala Pro Pro Ala Gly Tyr Gly Ala Pro Pro Leu Gly Tyr



115		120		125
Gly Ala Pro Pro Leu Gly Tyr Gly Thr Pro Pro Leu Gly Tyr Gly Ala				
130		135		140
Pro Pro Leu Gly Tyr Gly Ala Pro Pro Ala Gly Asn Glu Gly Pro Pro				
145		150		155
				160
Ala Gly Tyr Arg Ala Ser Pro Ala Gly Ser Gly Ala Arg Pro Gln Glu				
	165		170	175
Ser Thr Ala Ala Gln Ala Pro Glu Asn Glu Ala Ser Leu Pro Ser Ala				
	180		185	190
Ser Ser Ser Gln Asp Lys Glu Asp Asp Ser Gly Gln Pro Phe Leu Arg				
	195		200	205
Lys Ser Ala Phe Gln Cys Leu Leu Glu Cys Asp Asp Tyr Leu Ile Val				
	210		215	220

Arg  
225

<210> 11  
<211> 1001  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(708)  
<223>

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1	5	10
		15
gct gca aac ttc att aag gga act att cag gca gct cca tat ggt ggc		96
Ala Ala Asn Phe Ile Lys Gly Thr Ile Gln Ala Ala Pro Tyr Gly Gly		
	20	25
		30
tgg gaa gga caa gct act ttt aaa tta gtc ttc aga aat gga gat gcc		144
Trp Glu Gly Gln Ala Thr Phe Lys Leu Val Phe Arg Asn Gly Asp Ala		

35	40	45	
att gaa ttt gcc cag ttg atg gtg aaa gct gcc tct gct gtt gcc cga Ile Glu Phe Ala Gln Leu Met Val Lys Ala Ala Ser Ala Val Ala Arg 50 55 60			192
gga ttt cca ctt aga acc tta aat gac tgg ttc agc tct atg gga att Gly Phe Pro Leu Arg Thr Leu Asn Asp Trp Phe Ser Ser Met Gly Ile 65 70 75 80			240
tat gta att act ggg gaa ggg aat atg tgc act cca cag atg cct tgt Tyr Val Ile Thr Gly Glu Gly Asn Met Cys Thr Pro Gln Met Pro Cys 85 90 95			288
tca gtt att gtc tat ggg gcc cca cct gca gga tat gga gcc cca cct Ser Val Ile Val Tyr Gly Ala Pro Pro Ala Gly Tyr Gly Ala Pro Pro 100 105 110			336
ccc gga tac gga gcc cca cct gca gga tat gga gcc caa ccc gta gga Pro Gly Tyr Gly Ala Pro Pro Ala Gly Tyr Gly Ala Gln Pro Val Gly 115 120 125			384
aat gaa ggc ccg cct gtg gga tac aga gcc tca cct gtg cga tat gga Asn Glu Gly Pro Pro Val Gly Tyr Arg Ala Ser Pro Val Arg Tyr Gly 130 135 140			432
gcc cca cct ctt gga tac gga gcc cca cct gca gga tat gga gcc cca Ala Pro Pro Leu Gly Tyr Gly Ala Pro Pro Ala Gly Tyr Gly Ala Pro 145 150 155 160			480
cct cta gga tat gga gcc cca cct ctt gga tat gga acc cca cct ctc Pro Leu Gly Tyr Gly Ala Pro Pro Leu Gly Tyr Gly Thr Pro Pro Leu 165 170 175			528
gga tat gga gcc cca cct ctc gga tat gga gcc cca cct gca gga aat Gly Tyr Gly Ala Pro Pro Leu Gly Tyr Gly Ala Pro Pro Ala Gly Asn 180 185 190			576
gaa ggc ccg cct gcg gga tac aga gcc tca cct gct gga tca gga gcc Glu Gly Pro Pro Ala Gly Tyr Arg Ala Ser Pro Ala Gly Ser Gly Ala 195 200 205			624
agg cct cag gaa tct aca gca gcc cag gct cct gaa aac gag gct tct Arg Pro Gln Glu Ser Thr Ala Ala Gln Ala Pro Glu Asn Glu Ala Ser 210 215 220			672
ctt ccc tct gcc tcc tct tct cag gtc cat tct taa ccttctaaga Leu Pro Ser Ala Ser Ser Ser Gln Val His Ser 225 230 235			718
tgtaaaccctt gaagactcac caagcaaaga ggtaccctaa aattgaagtc aggataagga			778
ggacgactca gcttagagtc attgattgat ctgcattgtg aaaattagga aaccagatgc			838
tcccatgttc tcaaggacga cctttcttaa ggaagtcagt acgtgggcaa cagtgatgag			898
aggaagagag gagagactca accaactaga gcagggataa ggtttccctt gttcagcttt			958
tcagtgtctg ctggaatgtg atgattacct cattgtcagg tag			1001

<211> 235

<212> PRT

<213> Homo sapiens

<400> 12

Met Pro Phe Asp Leu Met Thr Asn Leu Thr Val Glu Gln Pro Val Phe  
1 5 10 15

Ala Ala Asn Phe Ile Lys Gly Thr Ile Gln Ala Ala Pro Tyr Gly Gly  
20 25 30

Trp Glu Gly Gln Ala Thr Phe Lys Leu Val Phe Arg Asn Gly Asp Ala  
35 40 45

Ile Glu Phe Ala Gln Leu Met Val Lys Ala Ala Ser Ala Val Ala Arg  
50 55 60

Gly Phe Pro Leu Arg Thr Leu Asn Asp Trp Phe Ser Ser Met Gly Ile  
65 70 75 80

Tyr Val Ile Thr Gly Glu Gly Asn Met Cys Thr Pro Gln Met Pro Cys  
85 90 95

Ser Val Ile Val Tyr Gly Ala Pro Pro Ala Gly Tyr Gly Ala Pro Pro  
100 105 110

Pro Gly Tyr Gly Ala Pro Pro Ala Gly Tyr Gly Ala Gln Pro Val Gly  
115 120 125

Asn Glu Gly Pro Pro Val Gly Tyr Arg Ala Ser Pro Val Arg Tyr Gly  
130 135 140

Ala Pro Pro Leu Gly Tyr Gly Ala Pro Pro Ala Gly Tyr Gly Ala Pro  
145 150 155 160

Pro Leu Gly Tyr Gly Ala Pro Pro Leu Gly Tyr Gly Thr Pro Pro Leu  
165 170 175

Gly Tyr Gly Ala Pro Pro Leu Gly Tyr Gly Ala Pro Pro Ala Gly Asn  
180 185 190

Glu Gly Pro Pro Ala Gly Tyr Arg Ala Ser Pro Ala Gly Ser Gly Ala  
195 200 205

AI

Arg Pro Gln Glu Ser Thr Ala Ala Gln Ala Pro Glu Asn Glu Ala Ser  
210 215 220

Leu Pro Ser Ala Ser Ser Ser Gln Val His Ser  
225 230 235

<210> 13

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 13  
ggcagggatg gcagtgaacc ag

22

<210> 14

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 14  
gtccatttac caccttctca gag

23

<210> 15

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 15  
atgccatttg atctgatg

18

A1

<210> 16  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer  
 <400> 16  
 atggagtaac agtccatc

18

<210> 17  
 <211> 166  
 <212> PRT  
 <213> Mus sp.

<400> 17

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 Asn Thr Glu Ser Ile Leu Met Ser Tyr Asp His Val Glu Leu Thr Phe  
 20 25 30  
 Asn Asp Met Lys Asn Val Pro Glu Ala Phe Lys Gly Thr Lys Lys Gly  
 35 40 45  
 Thr Val Tyr Leu Thr Pro Tyr Arg Val Ile Phe Leu Ser Lys Gly Lys  
 50 55 60  
 Asp Ala Met Gln Ser Phe Met Met Pro Phe Tyr Leu Met Lys Asp Cys  
 65 70 75 80  
 Glu Ile Lys Gln Pro Val Phe Gly Ala Asn Phe Ile Lys Gly Ile Val  
 85 90 95  
 Lys Ala Glu Ala Gly Gly Gly Trp Glu Gly Ser Ala Ser Tyr Lys Leu  
 100 105 110  
 Thr Phe Thr Ala Gly Gly Ala Ile Glu Phe Gly Gln Arg Met Leu Gln  
 115 120 125

A1

Val Ala Ser Gln Ala Ser Arg Gly Glu Val Pro Asn Gly Ala Tyr Gly  
130 135 140

Tyr Pro Tyr Met Pro Ser Gly Ala Tyr Val Phe Pro Pro Pro Val Ala  
145 150 155 160

Asn Gly Met Tyr Pro Cys  
165

<210> 18

<211> 359

<212> PRT

<213> Mus sp.

<400> 18

Met Ala Val Asn Gln Asn His Thr Val Asp Arg Arg Trp Ala Ala Ile  
1 5 10 15

Pro His Gly Glu Ser Leu Leu Lys Lys Cys Ser Glu Val Asp Leu Ser  
20 25 30

Phe Pro Gln Ser Pro Pro Gly Ser Asn Leu Phe Ser Gly Thr Lys Arg  
35 40 45

Gly Ala Leu Phe Leu Thr Ser Tyr Arg Val Ile Phe Val Thr Ser Arg  
50 55 60

Ala Asp Asn Asp Pro Met Phe Ser Phe Thr Met Pro Phe His Leu Met  
65 70 75 80

Asn Asn Cys Thr Val Glu Gln Pro Ile Phe Gly Ala Asn Tyr Ile Lys  
85 90 95

Gly Thr Ile Gln Ala Ala Pro Asp Gly Gly Trp Glu Gly Ser Ala Thr  
100 105 110

Phe Lys Ile Val Phe Arg Lys Gly Gly Ala Ile Asp Phe Ala Gln Leu  
115 120 125

Met Ala Lys Ala Ala Ser Ala Ala Ala Gln Gly Val Pro Leu Arg Val  
130 135 140

Ala Ser Phe Trp Met Gly Pro Leu Gly Ile Tyr Val Ile Thr Gly Asp  
145 150 155 160

Al

Arg Asn Met Tyr Ala Pro Gln Ala Tyr Gln Val Ala Tyr Gly Ala Pro  
165 170 175.

Pro Ala Gly Tyr Gly Ala Ser Pro Val Gly Tyr Gly Val Pro Ser Ala  
180 185 190

Gly Tyr Gly Ala Pro Pro Ala Gly Tyr Gly Ala Pro Pro Val Gly Tyr  
195 200 205

Val Ala Pro Ser Pro Gly Tyr Asp Val Leu Pro Pro Gly Tyr Gly Ala  
210 215 220

Val Arg Tyr Gly Ser Pro Pro Pro Leu Tyr Val Ala Thr Pro Met Gly  
225 230 235 240

Tyr Gly Val Pro Pro Pro Gly Tyr Gly Pro Pro Pro Val Arg Tyr Gly  
245 250 255

Ser Pro Pro Pro Gly Tyr Glu Ala Pro Thr Met Glu Tyr Gly Ala Gln  
260 265 270

Pro Pro Arg Tyr Gly Thr Thr Pro Met Gly Ser Gly Ser Pro Pro Pro  
275 280 285

Arg Tyr Glu Ala Pro Pro Met Gly Tyr Gly Thr Pro Pro Ser Gly Arg  
290 295 300

Glu Ser Ile Pro Pro Gly Ser Arg Ala Thr Ser Val Ala Gln Glu Ala  
305 310 315 320

Pro Pro Ala Gly Ser Glu Ala Gly His Pro Met Ser Val Ala Val Gln  
325 330 335

Asn Pro Glu Phe Gln Ala Ser Phe Pro Ser Thr Ser Ser Ser Gln Val  
340 345 350

His Ser Pro Arg Ser Lys Met  
355

<210> 19

<211> 171

<212> PRT

<213> Bos sp.

A1

<400> 19

Met Ala Val Asn Gln Ser His Thr Glu Ser Arg Arg Gly Ala Leu Ile  
1 5 10 15

Pro Ser Gly Glu Ser Val Leu Lys Gln Cys Glu Asp Val Asp Leu Cys  
20 25 30

Phe Leu Gln Lys Pro Val Glu Ser Tyr Leu Phe Asn Gly Thr Lys Lys  
35 40 45

Gly Thr Leu Phe Leu Thr Ser Tyr Arg Val Val Phe Val Thr Ser His  
50 55 60

Leu Val Asn Asp Pro Met Leu Ser Phe Met Met Pro Phe Gly Leu Met  
65 70 75 80

Ser Asp Cys Thr Ile Glu Gln Pro Ile Phe Ala Pro Asn Tyr Ile Lys  
85 90 95

Gly Thr Ile Gln Ala Ala Pro Gly Gly Gly Trp Glu Gly Gln Ala Val  
100 105 110

Phe Lys Leu Ser Phe Arg Lys Gly Gly Ala Ile Glu Phe Ala Gln Leu  
115 120 125

Met Val Lys Ala Ala Ser Ala Ala Ala Arg Gly Ile Pro Leu Gly Ser  
130 135 140

Val Asn Tyr Trp Phe Asp Thr Ser Gly Leu Tyr Ile Ile Thr Val Pro  
145 150 155 160

Gly Ala Ala Val Cys Ser Ser Gln Thr Pro Cys  
165 170

<210> 20

<211> 541

<212> PRT

<213> mammalian

<400> 20

Met Gly Cys Ile Lys Ser Lys Glu Asp Lys Gly Pro Ala Met Lys Tyr  
1 5 10 15

A1



Arg Thr Asp Asn Thr Pro Glu Pro Ile Ser Ser His Val Ser His Tyr  
20 25 30

Gly Ser Asp Ser Ser Gln Ala Thr Gln Ser Pro Ala Ile Lys Gly Ser  
35 40 45

Ala Val Asn Phe Asn Ser His Ser Met Thr Pro Phe Gly Gly Pro Ser  
50 55 60

Gly Met Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Ala Val Pro  
65 70 75 80

Ser Pro Tyr Pro Ser Thr Leu Thr Gly Gly Val Thr Val Phe Val Ala  
85 90 95

Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Asp Asp Leu Ser Phe Lys Lys  
100 105 110

Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp Trp Glu  
115 120 125

Ala Arg Ser Ile Ala Thr Gly Lys Thr Gly Tyr Ile Pro Ser Asn Tyr  
130 135 140

Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys  
145 150 155 160

Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu Asn Pro Gly Asn Gln  
165 170 175

Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr  
180 185 190

Ser Leu Ser Ile Arg Asp Trp Asp Glu Val Arg Gly Asp Asn Val Lys  
195 200 205

His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly Tyr Tyr Ile Thr Thr  
210 215 220

Arg Ala Gln Phe Glu Ser Leu Gln Lys Leu Val Lys His Tyr Arg Glu  
225 230 235 240

His Ala Asp Gly Leu Cys His Lys Leu Thr Thr Val Cys Pro Thr Val  
245 250 255

Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg  
260 265 270

A1

Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu  
275 280 285

Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala Ile Lys Thr  
290 295 300

Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu Ala Gln  
305 310 315 320

Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu Tyr Ala Val  
325 330 335

Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe Met Thr Lys Gly  
340 345 350

Ser Leu Leu Asp Phe Leu Lys Glu Gly Glu Gly Lys Phe Leu Lys Leu  
355 360 365

Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met Ala Tyr  
370 375 380

Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile  
385 390 395 400

Leu Val Gly Asp Asn Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala  
405 410 415

Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe  
420 425 430

Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr  
435 440 445

Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val  
450 455 460

Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu  
465 470 475 480

Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly Cys Pro  
485 490 495

Glu Ser Leu His Glu Leu Met Lys Leu Cys Trp Lys Lys Asp Pro Asp  
500 505 510

Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp Tyr Phe

515

520

.525

AI

Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Asp Asn Leu  
530 535 540

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